



## SEQUENCE LISTING

<110> SHERMAN, LINDA A.  
LUSTGARTEN, JOSEPH

<120> RECOMBINANT CONSTRUCTS ENCODING T CELL RECEPTORS  
SPECIFIC FOR HUMAN HLA-RESTRICTED TUMOR ANTIGENS

<130> 48340/55793-DIV

<140> 09/774,681

<141> 2001-02-01

<150> 08/812,393

<151> 1997-03-05

<150> 60/012,845

<151> 1996-03-05

<160> 65

<170> PatentIn Ver. 3.2

<210> 1

<211> 1350

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1332)

<220>

<223> Description of Artificial Sequence: Synthetic  
single chain TCR derivative nucleotide sequence

<400> 1

ctc	gag	atg	cag	agg	aac	ctg	gga	gct	gtg	ctg	ggg	att	ctg	tgg	gtg	48
Leu	Glu	Met	Gln	Arg	Asn	Leu	Gly	Ala	Val	Leu	Gly	Ile	Leu	Trp	Val	
1				5					10					15		

cag	att	tgc	tgg	ctg	aaa	gaa	cag	caa	gtg	cag	cag	agt	ccc	gca	tcc	96
Gln	Ile	Cys	Trp	Leu	Lys	Glu	Gln	Gln	Val	Gln	Gln	Ser	Pro	Ala	Ser	
			20					25					30			

ttg	gtt	ctg	cag	gag	ggg	gag	aac	gca	gag	ctc	cag	tgt	agc	ttt	tcc	144
Leu	Val	Leu	Gln	Glu	Gly	Glu	Asn	Ala	Glu	Leu	Gln	Cys	Ser	Phe	Ser	
		35					40					45				

atc	ttt	aca	aac	cag	gtg	cag	tgg	ttt	tac	caa	cgt	cct	ggg	gga	aga	192
Ile	Phe	Thr	Asn	Gln	Val	Gln	Trp	Phe	Tyr	Gln	Arg	Pro	Gly	Gly	Arg	
	50					55					60					

ctc	gtc	agc	ctg	ttg	tac	aat	cct	tct	ggg	aca	aag	cag	agt	ggg	aga	240
Leu	Val	Ser	Leu	Leu	Tyr	Asn	Pro	Ser	Gly	Thr	Lys	Gln	Ser	Gly	Arg	
65					70					75					80	

ctg aca tcc aca aca gtc att aaa gaa cgt cgc agc tct ttg cac att	288
Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile	
85 90 95	
tcc tcc tcc cag atc aca gac tca ggc act tat ctc tgt gcc tca aat	336
Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn	
100 105 110	
tct gga gga agc aat gca aag cta acc ttc ggg aaa ggc act aaa ctc	384
Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu	
115 120 125	
tct gtt aaa tca ggt ggc gga ggg tct ggc ggg ggt gga tcc ggg ggt	432
Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
130 135 140	
gga ggc tca gag gct gca gtc acc caa agc cca aga aac aag gtg gca	480
Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala	
145 150 155 160	
gta aca gga gga aag gtg aca ttg agc tgt aat cag act aat aac cac	528
Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His	
165 170 175	
aac aac atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg	576
Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu	
180 185 190	
atc cat tat tca tat ggt gct ggc agc act gag aaa gga gat atc cct	624
Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro	
195 200 205	
gat gga tac aag gcc tcc aga cca agc caa gag aac ttc tcc ctc att	672
Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile	
210 215 220	
ctg gag ttg gct acc ccc tct cag aca tca gtg tac ttc tgt gcc agc	720
Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser	
225 230 235 240	
ggt gag aca ggg acc aac gaa aga tta ttt ttc ggt cat gga acc aag	768
Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys	
245 250 255	
ctg tct gtc ctg act agt aac tcc atc atg tac ttc agc cac ttc gtg	816
Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val	
260 265 270	
ccg gtc ttc ctg cca gcg aag ccc acc acg acg cca gcg ccg cga cca	864
Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro	
275 280 285	
cca aca ccg gcg ccc acc atc gcg tcg cag ccc ctg tcc ctg cgc cca	912
Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro	
290 295 300	

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tct agt tct aga gat ccc aaa ctc tgc tac ctg ctg gat gga atc ctc 960
Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu
305                      310                      315                      320

ttc atc tat ggt gtc att ctc act gcc ttg ttc ctg aga gtg aag ttc 1008
Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe
                      325                      330                      335

agc agg agc gca gac gcc ccc gcg tac cag cag ggc cag aac cag ctc 1056
Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
                      340                      345                      350

tat aac gag ctc aat cta gga cga aga gag gag tac gat gtt ttg gac 1104
Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
                      355                      360                      365

aag aga cgt ggc cgg gac cct gag atg ggg gga aag ccg aga agg aag 1152
Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
370                      375                      380

aac cct cag gaa ggc ctg tac aat gaa ctg cag aaa gat aag atg gcg 1200
Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
385                      390                      395                      400

gag gcc tac agt gag att ggg atg aaa ggc gag cgc cgg agg ggc aag 1248
Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                      405                      410                      415

ggg cac gat ggc ctt tac cag ggt ctc agt aca gcc acc aag gac acc 1296
Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                      420                      425                      430

tac gac gcc ctt cac atg cag gcc ctg ccc cct cgc taa gcg gcc gcc 1344
Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                      435                      440

acc gcg 1350

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<210> 2

<211> 444

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
single chain TCR protein

<400> 2

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Leu Glu Met Gln Arg Asn Leu Gly Ala Val Leu Gly Ile Leu Trp Val
 1                      5                      10                      15

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Gln Ile Cys Trp Leu Lys Glu Gln Gln Val Gln Gln Ser Pro Ala Ser
 20                      25                      30

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Leu Val Leu Gln Glu Gly Glu Asn Ala Glu Leu Gln Cys Ser Phe Ser
 35                      40                      45

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Ile Phe Thr Asn Gln Val Gln Trp Phe Tyr Gln Arg Pro Gly Gly Arg  
 50 55 60  
 Leu Val Ser Leu Leu Tyr Asn Pro Ser Gly Thr Lys Gln Ser Gly Arg  
 65 70 75 80  
 Leu Thr Ser Thr Thr Val Ile Lys Glu Arg Arg Ser Ser Leu His Ile  
 85 90 95  
 Ser Ser Ser Gln Ile Thr Asp Ser Gly Thr Tyr Leu Cys Ala Ser Asn  
 100 105 110  
 Ser Gly Gly Ser Asn Ala Lys Leu Thr Phe Gly Lys Gly Thr Lys Leu  
 115 120 125  
 Ser Val Lys Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 130 135 140  
 Gly Gly Ser Glu Ala Ala Val Thr Gln Ser Pro Arg Asn Lys Val Ala  
 145 150 155 160  
 Val Thr Gly Gly Lys Val Thr Leu Ser Cys Asn Gln Thr Asn Asn His  
 165 170 175  
 Asn Asn Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu  
 180 185 190  
 Ile His Tyr Ser Tyr Gly Ala Gly Ser Thr Glu Lys Gly Asp Ile Pro  
 195 200 205  
 Asp Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile  
 210 215 220  
 Leu Glu Leu Ala Thr Pro Ser Gln Thr Ser Val Tyr Phe Cys Ala Ser  
 225 230 235 240  
 Gly Glu Thr Gly Thr Asn Glu Arg Leu Phe Phe Gly His Gly Thr Lys  
 245 250 255  
 Leu Ser Val Leu Thr Ser Asn Ser Ile Met Tyr Phe Ser His Phe Val  
 260 265 270  
 Pro Val Phe Leu Pro Ala Lys Pro Thr Thr Thr Pro Ala Pro Arg Pro  
 275 280 285  
 Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro  
 290 295 300  
 Ser Ser Ser Arg Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu  
 305 310 315 320  
 Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe  
 325 330 335  
 Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu  
 340 345 350

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp  
 355 360 365  
 Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys  
 370 375 380  
 Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala  
 385 390 395 400  
 Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys  
 405 410 415  
 Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr  
 420 425 430  
 Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg  
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<210> 3  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 3  
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24

<210> 4  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 4  
 tgagacaaag tccccaatct ctgacag

27

<210> 5  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 5  
 ctgcagctgc tcctcaagta ctattc

26

<210> 6  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 6  
 tcccggagaa ggtccacagt tcctcttt

28

<210> 7  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 7  
 gaagcagcag agggtttgaa gccacatac

29

<210> 8  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 8  
 ggcaggtctt cagttgctta tgaagggt

27

<210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 9  
 ggctcctctt cagggtccag aatatgt

27

<210> 10  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 10  
gcgaagaact caccctggac tgttcat

27

<210> 11  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 11  
gagctccaca gacaacaaga ggacgcagca

30

<210> 12  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 12  
gagctgcgac gttccttagt gactgtg

27

<210> 13  
<211> 30  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 13  
cctcgtcagc ctgttgtcca atccttctgg

30

<210> 14  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 14  
cagcctcatc aatctgttct acttggt

28

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 15  
 ccaccaggga ccacagttta tcattcaa 28  
  
 <210> 16  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 16  
 acctggagag aatcctaagc tcatcat 27  
  
 <210> 17  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 17  
 aggtcttggtg tccctgacag tcctggtt 28  
  
 <210> 18  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 18  
 caagcaaaca ctgtagtgca gagcccttcc 30  
  
 <210> 19  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: Primer  
  
 <400> 19  
 caagacatcc ataactgccc tacag 25  
  
 <210> 20  
 <211> 27



<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 20  
 gtgtatgaaa cccaggacag ttcttac

27

<210> 21  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 21  
 ccgtatttct ttcttatggt gttttggat

29

<210> 22  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 22  
 caaagctctc catcgctgac tgttcaag

28

<210> 23  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 23  
 atctaatacct gggaagagca aat

23

<210> 24  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 24  
 ggcgctcgtt accacgtggt caa

23

<210> 25  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 25  
 gtgaaagggc aaggacaaaa agc 23

<210> 26  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 26  
 gatatgcgaa cagtatctag gc 22

<210> 27  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 27  
 acataatcaa aggaaagga gaa 23

<210> 28  
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 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 28  
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<210> 29  
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<220>  
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<400> 29  
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<210> 30  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 30  
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<210> 31  
 <211> 23  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 31  
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<210> 32  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 32  
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<210> 33  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
 agcttgcaag agttggaaaa cca 23

<210> 34  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 34  
 gattatgttt agctacaata ata 23

<210> 35  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 35  
 acaaggtgac aggaaggga caa 23

<210> 36  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 36  
 acctacagaa cccaaggact cag 23

<210> 37  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 37  
 cagttgccct cggatcgatt ttc 23

<210> 38  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 38  
 gccgagatca aggctgtggg cag 23

<210> 39  
 <211> 23

<212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 39  
 agaaccatct gtaagagtgg aac 23

<210> 40  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 40  
 catcaaataa tagatatggg gca 23

<210> 41  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 41  
 gtagtcctga aaaagggcac act 23

<210> 42  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 42  
 catctgtcaa agtggcactt ca 22

<210> 43  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(393)

&lt;400&gt; 43

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Met	Lys	Ser	Leu	Ser	Val	Ser	Leu	Val	Val	Leu	Trp	Leu	Gln	Leu	Asn	
1				5					10					15		
tgg	gtg	cag	agc	cag	cag	aag	gtg	cag	cag	agc	cca	gaa	tcc	ctc	agt	96
Trp	Val	Gln	Ser	Gln	Gln	Lys	Val	Gln	Gln	Ser	Pro	Glu	Ser	Leu	Ser	
			20					25					30			
gtc	cca	gag	gga	ggc	atg	gcc	tct	ctc	aac	tgc	act	tca	agt	gat	cgc	144
Val	Pro	Glu	Gly	Gly	Met	Ala	Ser	Leu	Asn	Cys	Thr	Ser	Ser	Asp	Arg	
		35					40					45				
aat	ttt	cag	tat	ttc	tgg	tgg	tac	aga	cag	cat	tct	gga	gaa	ggc	ccc	192
Asn	Phe	Gln	Tyr	Phe	Trp	Trp	Tyr	Arg	Gln	His	Ser	Gly	Glu	Gly	Pro	
	50					55					60					
aaa	gca	ctg	atg	tcc	atc	ttc	tct	gat	ggg	gac	aag	aaa	gaa	ggc	aga	240
Lys	Ala	Leu	Met	Ser	Ile	Phe	Ser	Asp	Gly	Asp	Lys	Lys	Glu	Gly	Arg	
65					70				75						80	
ttc	aca	gct	cac	ctc	aat	aag	gcc	agc	ctg	cat	gtt	tcc	ctg	cac	atc	288
Phe	Thr	Ala	His	Leu	Asn	Lys	Ala	Ser	Leu	His	Val	Ser	Leu	His	Ile	
				85					90					95		
aga	gac	tcc	cag	ccc	agt	gac	tcc	gct	ctc	tac	ttc	tgt	gca	gtt	atg	336
Arg	Asp	Ser	Gln	Pro	Ser	Asp	Ser	Ala	Leu	Tyr	Phe	Cys	Ala	Val	Met	
			100					105					110			
gat	tat	aac	cag	ggg	aag	ctt	atc	ttt	ggg	cag	ggg	acc	aag	tta	tct	384
Asp	Tyr	Asn	Gln	Gly	Lys	Leu	Ile	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Ser	
		115					120					125				
atc	aag	ccc														393
Ile	Lys	Pro														
130																

&lt;210&gt; 44

&lt;211&gt; 131

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 44

Met	Lys	Ser	Leu	Ser	Val	Ser	Leu	Val	Val	Leu	Trp	Leu	Gln	Leu	Asn	
1				5					10					15		
Trp	Val	Gln	Ser	Gln	Gln	Lys	Val	Gln	Gln	Ser	Pro	Glu	Ser	Leu	Ser	
			20					25					30			
Val	Pro	Glu	Gly	Gly	Met	Ala	Ser	Leu	Asn	Cys	Thr	Ser	Ser	Asp	Arg	
		35					40					45				
Asn	Phe	Gln	Tyr	Phe	Trp	Trp	Tyr	Arg	Gln	His	Ser	Gly	Glu	Gly	Pro	
	50					55					60					

Lys Ala Leu Met Ser Ile Phe Ser Asp Gly Asp Lys Lys Glu Gly Arg  
 65 70 75 80  
 Phe Thr Ala His Leu Asn Lys Ala Ser Leu His Val Ser Leu His Ile  
 85 90 95  
 Arg Asp Ser Gln Pro Ser Asp Ser Ala Leu Tyr Phe Cys Ala Val Met  
 100 105 110  
 Asp Tyr Asn Gln Gly Lys Leu Ile Phe Gly Gln Gly Thr Lys Leu Ser  
 115 120 125  
 Ile Lys Pro  
 130

<210> 45  
 <211> 402  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(402)

<400> 45  
 atg ggc tcc aga ctc ttc ttt gtg gtt ttg att ctc ctg tgt gca aaa 48  
 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys  
 1 5 10 15  
 cac atg gag gct gca gtc acc caa agt cca aga agc aag gtg gca gta 96  
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val  
 20 25 30  
 aca gga gga aag gtg aca ttg agc tgt cac cag act aat aac cat gac 144  
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp  
 35 40 45  
 tat atg tac tgg tat cgg cag gac acg ggg cat ggg ctg agg ctg atc 192  
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile  
 50 55 60  
 cat tac tca tat gtc gct gac agc acg gag aaa gga gat atc cct gat 240  
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp  
 65 70 75 80  
 ggg tac aag gcc tcc aga cca agc caa gag aat ttc tct ctc att ctg 288  
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu  
 85 90 95  
 gag ttg gct tcc ctt tct cag tca gct gta tat ttc tgt gcc agc agc 336  
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser  
 100 105 110

gat ttc gcc ggg aca ggg ggc ttc tat gaa cag tac ttc ggt ccc ggc 384  
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly  
           115                          120                          125

acc agg ctc acg gtt tct 402  
 Thr Arg Leu Thr Val Ser  
           130

<210> 46  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 46  
 Met Gly Ser Arg Leu Phe Phe Val Val Leu Ile Leu Leu Cys Ala Lys  
   1                          5                          10                          15  
 His Met Glu Ala Ala Val Thr Gln Ser Pro Arg Ser Lys Val Ala Val  
                           20                          25                          30  
 Thr Gly Gly Lys Val Thr Leu Ser Cys His Gln Thr Asn Asn His Asp  
           35                          40                          45  
 Tyr Met Tyr Trp Tyr Arg Gln Asp Thr Gly His Gly Leu Arg Leu Ile  
           50                          55                          60  
 His Tyr Ser Tyr Val Ala Asp Ser Thr Glu Lys Gly Asp Ile Pro Asp  
   65                          70                          75                          80  
 Gly Tyr Lys Ala Ser Arg Pro Ser Gln Glu Asn Phe Ser Leu Ile Leu  
                           85                          90                          95  
 Glu Leu Ala Ser Leu Ser Gln Ser Ala Val Tyr Phe Cys Ala Ser Ser  
           100                          105                          110  
 Asp Phe Ala Gly Thr Gly Gly Phe Tyr Glu Gln Tyr Phe Gly Pro Gly  
           115                          120                          125  
 Thr Arg Leu Thr Val Ser  
           130

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           peptide

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<211> 9  
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1 5

<210> 54  
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Cys Leu Thr Ser Thr Val Gln Leu Val  
1 5

<210> 55  
<211> 9  
<212> PRT  
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<400> 55  
Gln Leu Met Pro Tyr Gly Cys Leu Leu  
1 5

<210> 56  
<211> 9  
<212> PRT  
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peptide

<400> 56  
Val Leu Val Lys Ser Pro Asn His Val  
1 5

<210> 57  
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<212> PRT  
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peptide

<400> 57  
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1 5

<210> 58  
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<400> 58  
Asp Leu Leu Glu Lys Gly Glu Arg Leu  
1 5

<210> 59  
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peptide

<400> 59  
Glu Leu Val Ser Glu Phe Ser Arg Met  
1 5

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<400> 63  
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Gly Gly Ser Ser Ser  
                   20